GAGGTGATAAAGCTTCACCAATGGGTGTACTGCTCACACAG (SEQ ID NO: 1)

was chosen to match sequences in the vector; and the reverse primer,

GTGGTGTATTGGTCTAGATCAATCAGAATCTGGGCACGGTTC (SEQ ID NO: 2)

corresponded to the last seven amino acids (i.e. amino acids 118-124) in the extracellular domain of CTLA4, and contained a restriction enzyme site, and a stop codon (TGA). The reverse primer specified a C120S (cysteine to serine at position 120) mutation. In particular, the nucleotide sequence GCA (nucleotides 34-36) of the reverse primer shown above is replaced with one of the following nucleotide sequences: AGA, GGA, TGA, CGA, ACT, or GCT. As persons skilled in the art will understand, the nucleotide sequence GCA is a reversed complementary sequence of the codon TGC for cysteine. Similarly, the nucleotide sequences AGA, GGA, TGA, CGA, ACT, or GCT are the reversed complementary sequences of the codons for serine. Polymerase chain reaction products were digested with *Hind*III/*Xba*I and directionally subcloned into the expression vector πLN (Bristol-Myers Squibb Company, Princeton, NJ). L104EA29YX$_{C120S}$ was prepared in an identical manner. Each construct was verified by DNA sequencing.

In the Claims:

Please amend the claims as follows:

-- 6. (Amended) The CTLA4 mutant molecule of claim 1 comprising methionine at position +1 and aspartic acid at position +124 as shown in Figure 7 (SEQ ID NO: 3 and 4).--

-- 7. (Amended) The CTLA4 mutant molecule of claim 1, comprising alanine at position -1 and aspartic acid at position +124 as shown in Figure 7 (SEQ ID NO: 3 and 4).--

-- 8. (Amended) The CTLA4 mutant molecule of claim 3, wherein the human immunoglobulin constant region is mutated to include a cysteine at position +130 substituted with a serine, a cysteine at position +136 substituted with a serine, a cysteine at position +139 substituted with a serine, and a proline at position +148 substituted with serine, as shown in Figure 7 (SEQ ID NO: 3 and 4).--

-- 9. (Amended) A soluble CTLA4 mutant molecule which binds with higher avidity to CD80 and/or CD86 than CTLA4, comprising an extracellular domain of CTLA4, wherein in the extracellular domain, alanine at position +29 is substituted with tyrosine and leucine at position +104 is substituted with glutamic acid as shown in Figure 7 (SEQ ID NO: 3 and 4).--

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-- 14. (Amended) The CTLA4 mutant molecule of claim 9 comprising methionine at position +1 and aspartic acid at position +124 as shown in Figure 7 (SEQ ID NO: 3 and 4).--

-- 15. (Amended) The CTLA4 mutant molecule of claim 9, comprising alanine at position -1 and aspartic acid at position +124 as shown in Figure 7 (SEQ ID NO: 3 and 4).--

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-- 16. (Amended) The CTLA4 mutant molecule of claim11, wherein the human immunoglobulin constant region is mutated to include a cysteine at position +130 substituted with a serine, a cysteine at position +136 substituted with a serine, a cysteine at position +139 substituted with a serine, and a proline at position +148 substituted with serine, as shown in Figure 7 (SEQ ID NO: 3 and 4).--

-- 17. (Amended) A soluble CTLA4 mutant molecule which binds with higher avidity to CD80 and/or CD86 than CTLA4, comprising an extracellular domain of CTLA4, wherein in the extracellular domain, leucine at position +104 is substituted with glutamic acid as shown in Figure 8 (SEQ ID NO: 5 and 6).--

-- 20. (Amended) The nucleic acid molecule of claim 18 having the nucleotide sequence beginning with adenine at nucleotide position +1 and ending with adenine at +1071 as shown in Figure 7 (SEQ ID NO: 3 and 4) or 8 (SEQ ID NO: 5 and 6).--

-- 21. (Amended) The nucleic acid molecule of claim 19 having the nucleotide sequence beginning with adenine at nucleotide position +1 and ending with adenine at +1071 as shown in Figure 7 (SEQ ID NO: 3 and 4) or 8 (SEQ ID NO: 5 and 6).--

-- 22. (Amended) The nucleic acid molecule of claim 18 having the nucleotide sequence beginning with guanidine at –3 and ending at adenine at +1071 as shown in Figure 7 (SEQ ID NO: 3 and 4) or 8 (SEQ ID NO: 5 and 6).--

-- 23. (Amended) The nucleic acid molecule of claim 18 having the nucleotide sequence beginning with guanidine at –3 and ending at adenine at +1071 as shown in Figure 7 (SEQ ID NO: 3 and 4) or 8 (SEQ ID NO: 5 and 6).--

-- 39. (Amended) The method of claim 37, wherein the soluble CTLA4 mutant molecule comprises an extracellular domain of CTLA4, wherein in the extracellular domain leucine at position +104 is substituted with glutamic acid as shown in Figure 8 (SEQ ID NO: 5 and 6).--

-- 48. (Amended) The method of claim 46, wherein the soluble CTLA4 mutant molecule comprises an extracellular domain of CTLA4, wherein in the extracellular domain,